

#73



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1 2 1600

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/828,995B

DATE: 02/28/2002

TIME: 13:15:50

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\02282002\I828995B.raw

3 <110> APPLICANT: Heska Corporation  
 4 McCall, Catherine A.  
 5 Tang, Liang A.  
 7 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IgG AND CANINE  
 IL-13 RECEPTORS  
 9 <130> FILE REFERENCE: AL-7  
 11 <140> CURRENT APPLICATION NUMBER: 09/828,995B  
 12 <141> CURRENT FILING DATE: 2001-04-09  
 14 <150> PRIOR APPLICATION NUMBER: 60/195,874  
 15 <151> PRIOR FILING DATE: 2000-04-07  
 17 <150> PRIOR APPLICATION NUMBER: 60/195,659  
 18 <151> PRIOR FILING DATE: 2000-04-07  
 20 <160> NUMBER OF SEQ ID NOS: 104  
 22 <170> SOFTWARE: PatentIn version 3.1  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 51  
 26 <212> TYPE: DNA  
 27 <213> ORGANISM: Canis familiaris  
 29 <220> FEATURE:  
 30 <221> NAME/KEY: CDS  
 31 <222> LOCATION: (1)..(51)  
 32 <223> OTHER INFORMATION:  
 35 <400> SEQUENCE: 1  
 36 ttc aat gaa tgc aga tgc act gat aca ccc cca tgc cca gtc cct gaa 48  
 37 Phe Asn Glu Cys Arg Cys Thr Asp Thr Pro Pro Cys Pro Val Pro Glu  
 38 1 5 10 15  
 40 cct 51  
 41 Pro  
 45 <210> SEQ ID NO: 2  
 46 <211> LENGTH: 17  
 47 <212> TYPE: PRT  
 48 <213> ORGANISM: Canis familiaris  
 50 <400> SEQUENCE: 2  
 52 Phe Asn Glu Cys Arg Cys Thr Asp Thr Pro Pro Cys Pro Val Pro Glu  
 53 1 5 10 15  
 56 Pro  
 60 <210> SEQ ID NO: 3  
 61 <211> LENGTH: 51  
 62 <212> TYPE: DNA  
 63 <213> ORGANISM: Canis familiaris  
 65 <400> SEQUENCE: 3  
 66 aggttcaggg actgggcatg ggggtgtatc agtgcacatg cattcattga a 51  
 69 <210> SEQ ID NO: 4  
 70 <211> LENGTH: 1654

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71 <212> TYPE: DNA
72 <213> ORGANISM: Canis familiaris
74 <220> FEATURE:
75 <221> NAME/KEY: CDS
76 <222> LOCATION: (70)..(1473)
77 <223> OTHER INFORMATION:
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81 ggcacgagcc agccccagg atccccagg gacccattc agtgctcagg acacaacaca      60
83 gacaccacc atg gag tct gtg ttc tgc tgg gtt ttc ctt gtc gtt att tta      111
84      Met Glu Ser Val Phe Cys Trp Val Phe Leu Val Val Ile Leu
85      1          5          10
87 aaa ggt gtc cag ggt gag gtg cag ttg gtg gag tct ggg gga gac ctg      159
88 Lys Gly Val Gln Gly Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu
89 15          20          25          30
91 gtg aag cct ggg ggg tcc ctg aga ctc tcc tgt gtg gcc tct gga ttc      207
92 Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe
93          35          40          45
95 acc ttc agt tcg tac tac atg cat tgg atc cgc cag gct cca ggg aag      255
96 Thr Phe Ser Ser Tyr Tyr Met His Trp Ile Arg Gln Ala Pro Gly Lys
97          50          55          60
99 ggg ctt cag cgg gtc gca cat att aga ggt gat gga agg act aca cac      303
100 Gly Leu Gln Arg Val Ala His Ile Arg Gly Asp Gly Arg Thr Thr His
101          65          70          75
103 tac gca gac gct atg aag ggc cga ttc acc atc tcc aga gac aac gcc      351
104 Tyr Ala Asp Ala Met Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
105          80          85          90
107 aag aac acg ctg tat ctg cag atg aat agc ctg aca gtc gaa gac acg      399
108 Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Thr Val Glu Asp Thr
109 95          100          105          110
111 gct att tat tac tgt gta aag gac ata tac tat ggg gtc ggg gac tat      447
112 Ala Ile Tyr Tyr Cys Val Lys Asp Ile Tyr Tyr Gly Val Gly Asp Tyr
113          115          120          125
115 tgg ggc cag gga acc ctg gtc acc gtc tcc tca gcc tcc acc acg gcc      495
116 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Thr Ala
117          130          135          140
119 ccc tcg gtt ttc cca ctg gcc ccc agc tgc ggg tcc act tcc ggc tcc      543
120 Pro Ser Val Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser
121          145          150          155
123 acg gtg gcc ctg gcc tgc ctg gtg tca ggc tac ttc ccc gag cct gta      591
124 Thr Val Ala Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val
125          160          165          170
127 act gtg tcc tgg aat tcc ggc tcc ttg acc agc ggt gtg cac acc ttc      639
128 Thr Val Ser Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe
129 175          180          185          190
131 ccg tcc gtc ctg cag tcc tca ggg ctt cac tcc ctc agc agc atg gtg      687
132 Pro Ser Val Leu Gln Ser Ser Gly Leu His Ser Leu Ser Ser Met Val
133          195          200          205
135 aca gtg ccc tcc agc agg tgg ccc agc gag acc ttc acc tgc aac gtg      735
136 Thr Val Pro Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val

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137				210				215				220					
139	gtc	cac	cca	gcc	agc	aac	act	aaa	gta	gac	aag	cca	gtg	ttc	aat	gaa	783
140	Val	His	Pro	Ala	Ser	Asn	Thr	Lys	Val	Asp	Lys	Pro	Val	Phe	Asn	Glu	
141			225					230					235				
143	tgc	aga	tgc	act	gat	aca	ccc	cca	tgc	cca	gtc	cct	gaa	cct	ctg	gga	831
144	Cys	Arg	Cys	Thr	Asp	Thr	Pro	Pro	Cys	Pro	Val	Pro	Glu	Pro	Leu	Gly	
145		240					245					250					
147	ggg	cct	tcg	gtc	ctc	atc	ttt	ccc	ccg	aaa	ccc	aag	gac	atc	ctc	agg	879
148	Gly	Pro	Ser	Val	Leu	Ile	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Ile	Leu	Arg	
149	255					260					265					270	
151	att	acc	cga	aca	ccc	gag	gtc	acc	tgt	gtg	gtg	tta	gat	ctg	ggc	cgt	927
152	Ile	Thr	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Leu	Asp	Leu	Gly	Arg	
153				275						280					285		
155	gag	gac	cct	gag	gtg	cag	atc	agc	tgg	ttc	gtg	gat	ggg	aag	gag	gtg	975
156	Glu	Asp	Pro	Glu	Val	Gln	Ile	Ser	Trp	Phe	Val	Asp	Gly	Lys	Glu	Val	
157			290						295				300				
159	cac	aca	gcc	aag	acc	cag	tct	cgt	gag	cag	cag	ttc	aac	ggc	acc	tac	1023
160	His	Thr	Ala	Lys	Thr	Gln	Ser	Arg	Glu	Gln	Gln	Phe	Asn	Gly	Thr	Tyr	
161			305					310					315				
163	cgt	gtg	gtc	agc	gtc	ctc	ccc	att	gag	cac	cag	gac	tgg	ctc	aca	ggg	1071
164	Arg	Val	Val	Ser	Val	Leu	Pro	Ile	Glu	His	Gln	Asp	Trp	Leu	Thr	Gly	
165		320					325					330					
167	aag	gag	ttc	aag	tgc	aga	gtc	aac	cac	ata	gac	ctc	ccg	tct	ccc	atc	1119
168	Lys	Glu	Phe	Lys	Cys	Arg	Val	Asn	His	Ile	Asp	Leu	Pro	Ser	Pro	Ile	
169	335				340						345				350		
171	gag	agg	acc	atc	tct	aag	gcc	aga	ggg	agg	gcc	cat	aag	ccc	agt	gtg	1167
172	Glu	Arg	Thr	Ile	Ser	Lys	Ala	Arg	Gly	Arg	Ala	His	Lys	Pro	Ser	Val	
173				355						360					365		
175	tat	gtc	ctg	ccg	cca	tcc	cca	aag	gag	ttg	tca	tcc	agt	gac	aca	gtc	1215
176	Tyr	Val	Leu	Pro	Pro	Ser	Pro	Lys	Glu	Leu	Ser	Ser	Ser	Asp	Thr	Val	
177			370						375					380			
179	agc	atc	acc	tgc	ctg	ata	aaa	gac	ttc	tac	cca	cct	gac	att	gat	gtg	1263
180	Ser	Ile	Thr	Cys	Leu	Ile	Lys	Asp	Phe	Tyr	Pro	Pro	Asp	Ile	Asp	Val	
181			385					390					395				
183	gag	tgg	cag	agc	aat	gga	cag	cag	gag	ccc	gag	agg	aag	cac	cgc	atg	1311
184	Glu	Trp	Gln	Ser	Asn	Gly	Gln	Gln	Glu	Pro	Glu	Arg	Lys	His	Arg	Met	
185		400				405						410					
187	acc	ccg	ccc	c													

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203 cccacccttg gctctcagga tccccgagg acacctgagc ccctgtccct gtgtacataa 1563
205 ccctgggtag gcacccatca tgaaataaag caccagcac tgccctgggc cctgcaaaaa 1623
207 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 1654
210 <210> SEQ ID NO: 5
211 <211> LENGTH: 468
212 <212> TYPE: PRT
213 <213> ORGANISM: Canis familiaris
215 <400> SEQUENCE: 5
217 Met Glu Ser Val Phe Cys Trp Val Phe Leu Val Val Ile Leu Lys Gly
218 1 5 10 15
221 Val Gln Gly Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys
222 20 25 30
225 Pro Gly Gly Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe
226 35 40 45
229 Ser Ser Tyr Tyr Met His Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu
230 50 55 60
233 Gln Arg Val Ala His Ile Arg Gly Asp Gly Arg Thr Thr His Tyr Ala
234 65 70 75 80
237 Asp Ala Met Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
238 85 90 95
241 Thr Leu Tyr Leu Gln Met Asn Ser Leu Thr Val Glu Asp Thr Ala Ile
242 100 105 110
245 Tyr Tyr Cys Val Lys Asp Ile Tyr Tyr Gly Val Gly Asp Tyr Trp Gly
246 115 120 125
249 Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Thr Ala Pro Ser
250 130 135 140
253 Val Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val
254 145 150 155 160
257 Ala Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr Val
258 165 170 175
261 Ser Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe Pro Ser
262 180 185 190
265 Val Leu Gln Ser Ser Gly Leu His Ser Leu Ser Ser Met Val Thr Val
266 195 200 205
269 Pro Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Val His
270 210 215 220
273 Pro Ala Ser Asn Thr Lys Val Asp Lys Pro Val Phe Asn Glu Cys Arg
274 225 230 235 240
277 Cys Thr Asp Thr Pro Pro Cys Pro Val Pro Glu Pro Leu Gly Gly Pro
278 245 250 255
281 Ser Val Leu Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr
282 260 265 270
285 Arg Thr Pro Glu Val Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp
286 275 280 285
289 Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr
290 290 295 300
293 Ala Lys Thr Gln Ser Arg Glu Gln Gln Phe Asn Gly Thr Tyr Arg Val
294 305 310 315 320
297 Val Ser Val Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu

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298          325          330          335
301 Phe Lys Cys Arg Val Asn His Ile Asp Leu Pro Ser Pro Ile Glu Arg
302          340          345          350
305 Thr Ile Ser Lys Ala Arg Gly Arg Ala His Lys Pro Ser Val Tyr Val
306          355          360          365
309 Leu Pro Pro Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Ser Ile
310          370          375          380
313 Thr Cys Leu Ile Lys Asp Phe Tyr Pro Pro Asp Ile Asp Val Glu Trp
314 385          390          395          400
317 Gln Ser Asn Gly Gln Gln Glu Pro Glu Arg Lys His Arg Met Thr Pro
318          405          410          415
321 Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser
322          420          425          430
325 Val Asp Lys Ser Arg Trp Gln Gln Gly Asp Pro Phe Thr Cys Ala Val
326          435          440          445
329 Met His Glu Thr Leu Gln Asn His Tyr Thr Asp Leu Ser Leu Ser His
330          450          455          460
333 Ser Pro Gly Lys
334 465
337 <210> SEQ ID NO: 6
338 <211> LENGTH: 1654
339 <212> TYPE: DNA
340 <213> ORGANISM: Canis familiaris
342 <400> SEQUENCE: 6
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345 gctttatttc atgatgggtg cctaccaggg gttatgtaca cagggacagg ggctcagggtg 120
347 tcctcagggg atcctgagag ccaaggggtg ggggcttgct ggggtgccgg cggtgttgctc 180
349 atttaccggg agaatgggag agggatagat ctgtgtagtg gttctgtaga gtttcatgca 240
351 tcaccgcaca tgtgaagggg tctccctgct gccagcggct cttgtccaca gagagcttgc 300
353 tgtacaggaa gtaggaccgc tctcgtcca gctggggcgg ggtcatgcgg tgcttctctc 360
355 cgggctcctg ctgtccattg ctctgccact ccacatcaat gtcagggtgg tagaagtctt 420
357 ttatcaggca ggtgatgctg actgtgtcac tggatgacaa ctcttttggg gatggcggca 480
359 ggacatacac actgggctta tgggcccctc ctctggcctt agagatggtc ctctcgatgg 540
361 gagacgggag gtctatgtgg ttgactctgc acttgaactc cttccctgtg agccagtcct 600
363 ggtgctcaat ggggaggagc ctgaccacac ggtaggtgcc gttgaactgc tgctcacgag 660
365 actgggtctt ggctgtgtgc acctccttac catccacgaa ccagctgatc tgcacctcag 720
367 ggtcctcagc gccagatctt aacaccacac aggtgacctc ggggtgttcgg gtaatcctga 780
369 ggatgtcctt gggtttcggg ggaaagatga ggaccgaagg ccctccaga ggttcaggga 840
371 ctgggcatgg ggggtgatca gtgcatctgc attcattgaa cactggcttg tctactttag 900
373 tgttgctggc tgggtggacc acgttgagg tgaaggcttc gctgggccac ctgctggagg 960
375 gcaactgtcac catgctgctg agggagtga ggcctgagga ctgcaggacg gacgggaagg 1020
377 tgtgcacacc gctggtcaag gagccggaat tccaggacac agttacaggc tcggggaagt 1080
379 agcctgacac caggcaggcc agggccaccg tggagccgga agtggaccgc cagctggggg 1140
381 ccagtgggaa aaccgagggg gccgtgggtg aggcgtgagga gacggtgacc agggttccct 1200
383 ggccccaata gtccccgacc ccatagtata tgtcctttac acagtaataa atagccgtgt 1260
385 cttogactgt caggctattc atctgcagat acagcgtgtt cttggcgttg tctctggaga 1320
387 tggatgaatc gcccttcata gcgctctgcgt agtgtgtagt ccttccatca cctctaata 1380
389 gtgcgacccg ctgaagcccc ttccttgagg cctggcggat ccaatgcatg tagtacgaac 1440
391 tgaaggtgaa tccagaggcc acacaggaga gtctcaggga cccccaggc ttcaccaggt 1500

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

## VERIFICATION SUMMARY

DATE: 02/28/2002

PATENT APPLICATION: US/09/828,995B

TIME: 13:15:51

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\02282002\I828995B.raw

L:829 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
L:1139 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:1588 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25  
L:1589 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25  
L:1597 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25  
L:1686 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
L:1690 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
L:1736 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27  
L:1827 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28  
L:1829 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28  
L:1907 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30  
L:1909 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30  
L:2726 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40  
L:2839 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48  
L:3458 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57  
L:3544 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59  
L:3699 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:60  
L:3823 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62  
L:5961 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:83  
L:5997 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:84  
L:6027 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85  
L:6057 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:86  
L:6093 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:87  
L:6117 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:88